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Genetic Evaluation of Young Boars and Gilts for Sow Productivity

ABSTRACT

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Evidence is provided that increases of up to 62 percent in the accuracy of estimating breeding values of young herd replacement candidates for sow productivity can be achieved by considering productivity records from the sire's side of the pedigree, in addition to records for the dam. This evidence is based on comparisons of expected correlations of the theoretical true breeding value of a candidate with its estimated breeding value computed from records for various combinations of ancestors. Practical guidelines and examples are given for on-the-farm application of recommended procedures to evaluate young breeding herd candidates, based on combining the estimated breeding values of their sires and dams. Equations to compute the required breeding values are derived according to current animal breeding theory.

KEYWORDS: Estimating breeding values, pedigree evaluation, sow productivity, swine selection, swine sire proofs.

CONTENTS

GENETIC EVALUATION OF YOUNG BOARS AND GILTS FOR SOW PRODUCTIVITY

by Ben Bereskin[1]

INTRODUCTION

Sow productivity generally is recognized as a key factor affecting the efficiency and economy of the swine enterprise for both the seed-stock and commercial producer. The most common measures of sow productivity are based on productivity either per farrowing or per year. Productivity per farrowing usually refers to such traits as number of live pigs farrowed and number of pigs and total litter weight at some standard age such as 21 days. These traits often are combined and expressed in the form of an index. Productivity per year generally refers to number of live pigs farrowed or weaned by a sow per year. In this publication, productivity per farrowing is considered the basis for evaluating the genetic merit of animals in a herd, whereas productivity per year is considered primarily as a basis for evaluating the herd management.

Use of Pedigree Information

Practically all programs currently being promoted to improve sow productivity by selection rely solely on productivity records of the dams of young boar and gilt candidates for the breeding herd. The sire's side of the pedigree, whose contribution to the genetic merit of the offspring essentially equals that of the dam, has largely been ignored.

This situation contrasts with that in the dairy industry, where full pedigree information has long been used in selecting young bulls to be tested for possible use in artificial insemination programs. The pedigree information has been very useful, as pedigree estimates of the breeding values of young bulls have generally been highly correlated with their ultimate proofs (Powell et al., 1977).[2] The largely successful application of pedigree information in dairy breeding suggests that comparable results can be achieved in selecting young boars and gilts as breeding herd replacements.

Maternal Effects

There is also some evidence that maternal effects, reflecting mainly the level of nourishment provided by the sow to her prenatal and her nursing litter, may affect the ultimate productivity of her daughters. For example, Robison (1981) reported that, on the average, gilts born and nursed in extra large litters may not be as productive as their dams. This finding may be a cause for the apparent low heritability of sow productivity traits or index.

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[2] The year after the author's name refers to Literature Cited, p. 16.

However, the sire does not directly influence his offspring by any maternal effects. Thus, in evaluating young animals for genetic merit, using records for the sire, along with those for the dam, would appear to significantly reduce possible bias from maternal effects.

Heritability Estimates

Two published studies, including records of grandparents in their computations, reported heritability estimates for measures of sow productivity to be .28 (Revelle and Robison, 1973) and .21 (Bereskin and Froblish, 1981). These values may more closely reflect higher direct genetic effects on sow productivity than previously considered. If confirmed, this finding suggests that genetic progress is possible from a comprehensive and sustained program of direct selection for measures of sow productivity. The proper evaluation and selection of young breeding herd candidates--boars and gilts-- is one area where producers can make significant progress in raising the level of sow productivity in their herds.

Objectives

The main objectives of this report are (1) to demonstrate the merits of considering records from the sire's side of the pedigree, in addition to records for the dam, in evaluating young breeding herd replacement candidates for sow productivity; (2) to provide practical guidelines and examples for implementing such a herd program; and (3) to present the derivation of various equations used in the evaluations.

The basis proposed here for evaluating and selecting young herd replacement candidates is their estimated breeding value (EBV) for an index of sow productivity. The EBV of an animal may be defined simply as the estimated average value of the genes the animal possesses. This value is expressed in the subsequent level of productivity by a gilt herself and (or) in the contributions of the genes to the offspring of the gilt or boar. Half of the genes are obtained from the dam and half from the sire of the candidate, and a sample half of the full complement of genes is passed on to each offspring.

Using Records of Ancestors

Because sow productivity is both a sex- and age-limited trait, not yet expressed in the young animal, evaluation must depend on records for ancestors and (or) sibs. However, sibs can be considered as progeny of ancestors. With ancestors, it is preferable to use records of the candidate's most immediate ancestors--its sire and dam. However, until an adequate number of daughters of the sire have been tested, records for the sire's parents can be substituted in computing the candidate's EBV.

The EBV of a candidate is basically determined by a selection index. Such an index includes records for particular ancestors along with coefficients or factors expressing the expected regression of the candidate's EBV on the records for the respective ancestors. The two types of such records are productivity records by the sow herself and productivity records by daughters of a boar. In each case, the records are expressed as deviations from the contemporary herd averages. The proof of a boar is defined here as the average of his daughters' deviations from their respective herd averages.

Advantages of Using Sire Information

First, we need to consider the advantages, if any, of including records from the sire's side of the pedigree, along with those for the dam, in evaluating young boars and gilts for sow productivity. The measure of accuracy used here is the expected correlation of the true breeding value of a candidate with its EBV derived from records for various combinations of ancestors. This correlation (R) is a measure of the reliability or accuracy of the EBV as a measure of the true breeding value. The larger the R-value, the more accurate and reliable is the EBV. The R-values are computed on the basis of current animal breeding theory. The pertinent equations are derived in the appendix.

Shown in table 1 are three sets of R-values based on records for (1) the dam alone, (2) the dam and a proof of the sire, and (3) the dam and the sire's dam (paternal granddam, PGD) and a proof of the paternal grandsire (PGS).

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Table 1.--Comparisons of expected correlations among various combinations of records

I. Expected correlation (R) of the true breeding value of a candidate with the breeding value estimated from records of its dam[1]

k	Number of records (n) for dam		
	1	2	3
4 ----------	.239	.275	.291
8 ----------	.252	.284	.298

(k = number of sows in contemporary herd average.)

II. Expected correlation (R) of the true breeding value of a candidate with the breeding value estimated from the combination of records for its dam and a proof for its sire[1]

N	n = 1		n = 2		n = 3	
	k = 4	k = 8	k = 4	k = 8	k = 4	k = 8
2 ----	.325(36%)	.342(36%)	.352(28%)	.366(29%)	.365(25%)	.377(27%)
4 ----	.364(52)	.380(51)	.388(41)	.402(42)	.400(37)	.412(38)
6 ----	.387(62)	.401(59)	.410(49)	.422(49)	.420(44)	.432(45)

(N = number of daughters in sire proof.)

III. Expected correlation (R) of the true breeding value of a candidate with the breeding value estimated from a combination of records for its dam and paternal granddam and a proof for its paternal grandsire[1]

N	n = 1		n = 2		n = 3	
	k = 4	k = 8	k = 4	k = 8	k = 4	k = 8
2 ----	.289(21%)	.304(21%)	.326(19%)	.338(19%)	.343(18%)	.353(18%)
4 ----	.300(26)	.315(25)	.336(22)	.348(23)	.353(21)	.362(21)
6 ----	.307(28)	.322(28)	.343(25)	.354(25)	.369(23)	.368(23)

[1] See text for further explanation.

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The R-values, computed from one, two, or three records of the dam alone, range from .239 for one record by the dam and four records in her contemporary herd average to .298 for three records by the dam and an average of eight records in her contemporary herd averages. These are base R-values with which most of the following comparisons are made.

When the proof of the sire is used, along with records for the dam, R is increased by 25 to 36 percent when the sire proof is based on only two daughters (table 1, part II). When the sire's proof is based on four daughters, the accuracy or reliability of the EBV is increased by 37 to 52 percent over use of the dam's records alone. Finally, when six daughters are included in the sire's proof, the accuracy of the EBV is increased by 44 to as much as 62 percent over that when only the dam's records are considered. These computations are based on equal numbers of records (k) in the herd averages for sows and daughters of boars.

Increasing the number of daughters in a boar's proof can be seen to have a much greater effect on the comparative R-values than increasing the number of herdmates in the contemporary herd averages. Also, increasing the number of records by a sow is more important, in terms of R-values, than increasing the number of contemporary herdmates.

Using Records for Paternal Grandparents

A major problem with using sire proofs in estimating the breeding value of a young breeding herd candidate is that often none of the sire's daughters has yet farrowed a litter in the herd. In that case, two alternatives are available for inclusion of information from the sire's side of the pedigree.

(1) Compute the EBV from records for the dam and paternal grandparents (PGD and PGS). The expected R-values are shown in table 1, part III, along with percentage increases in R-values over those from comparable dam records alone. In the computations it was assumed that the dam and PGD had the same number of records and that herd averages included the same number of records for all three ancestors.

The advantages of using records for the sire's parents are considerably less than the advantages of including the sire's proof, but they are still substantial in comparison with using records for the dam alone to compute the EBV. Increases in R range from 18 to 28 percent for the combinations of records shown. However, the increases in R would be even larger if the PGD had more records than the dam, a likely occurrence. (For example, see the next paragraph.)

(2) Compute the EBV for the candidate with records for the dam and PGD if a proof of the PGS is not available. With equal numbers of records and herdmates for the dam and PGD, R would be increased by 12 percent over use of the dam's records alone. Equation 13 in the appendix (p. 28) was used to compute R with records for the dam and PGD. If, as is likely, the PGD has more records than the dam, then including the PGD would be more advantageous. For example, with one record for the dam and two records for the PGD, the R-values from records for the dam and PGD would be 16 percent higher than the values from records for the dam alone.

Using Own Versus Parents' Records

An important question is when should a producer use the EBV for a sow, based on her own record, and the EBV for a boar, based on his own proof, instead of relying on estimates from their parents? The R-values provide some answers.

The R-values for a sow's EBV, based on her own records, are exactly twice those shown for a dam (table 1, part I). Thus, with one record for the sow and four records in her contemporary herd average, $R = 2 \times .239 = .478$, and for $k = 8$, $R = 2 \times .252 = .504$. Both of these values are larger than any R-value based on sire + dam (table 1, part II). In other words, when the sow has farrowed and weaned her litter, her EBV should be computed from her own record and used in evaluating her progeny. This does not imply that records of ancestors should not be considered in evaluating sows with at least one productivity record of their own. However, that problem is not the subject of this publication.

The R-values for a boar's EBV, based on his own proof, are shown in table 2 for various combinations of daughters and herdmates. Each of the boar's R-values exceeds all those based on his dam's records (table 1, part I). Thus, a boar's EBV, even based on only two daughters, is more reliable than his EBV based on his dam's records for sow productivity. However, the boar's EBV must be based on at least six daughters before it is consistently more reliable than the EBV computed from records for his sire + dam (table 1, part II). The recommendation, therefore, is to wait until the boar has at least four tested daughters in the herd, and preferably six, before computing and using the EBV based on his own proof. The boar's EBV should be updated periodically as more daughters farrow and wean litters.

Conclusion

In these computations, only a small fraction of the many possible combinations of records was considered. However, the results are, in general, indicative of what might be expected in practice. It is therefore apparent that including information from the sire's side of the pedigree, in addition to

Table 2.--Expected correlation (R) of the true breeding value of a boar with his breeding value estimated from his proof[1]

N	k = 4	k = 8
2 ----------	.312	.326
4 ----------	.388	.402
6 ----------	.430	.442

[1] See text for further explanation.
(k = number of sows in contemporary herd average;
N = number of daughters in proof.)

records from the dam, would in most situations substantially increase the accuracy and reliability of the computed EBV's for young breeding herd candidates.

The task remains of presenting practical guidelines for easy application on the farm. The problem is not to compromise too freely the basic animal breeding concepts while devising procedures that are understood readily enough to be utilized on the farm by constructive breeders.

One of the major advantages of working with the estimated breeding value (EBV) is that it allows for an easy system of application in practice. This is because, as noted previously, the EBV represents the average value for the genes an animal possesses. Half of these genes are inherited from each parent, and a sample half of the full complement of the genes is then passed on to each offspring.

As a result, the EBV for any young breeding herd candidate can be computed simply as the average of the EBV's for its sire and dam. Until the sire has an adequate proof, the sire's EBV can be computed as the average of the EBV's for its own sire and dam (the PGS and PGD). The EBV for the candidate can then be computed as the simple average of the EBV's for its parents. When neither a candidate's sire nor PGS has a proof, the candidate's EBV can be computed as the average of its dam's EBV and one-half the EBV for its PGD. This assumes that the EBV for the PGS equals the herd average.

Only two basic equations are needed by the producer to compute the EBV for all animals in the herd. One equation is for sows that have farrowed and one equation is for boars that have daughters which have farrowed in the herd.

Computing the Sow's EBV

The following equation is recommended:

$$\text{EBV (Sow)} = \underbrace{\frac{n \, k \, h^2}{(1-s)(k+1)+k(n-1)(h^2+t)}}_{A} \underbrace{(\overline{\text{Sow} - \text{Herd average}})}_{B}. \quad [1]$$

Part A in equation [1] is the regression factor used to derive an estimate of the sow's EBV from the average of her productivity records, expressed as the average deviation from their respective contemporary herd averages (part B). A line over a term in an equation indicates an average for that term. It is proposed that each EBV be expressed as a percentage deviation, either + or -, from the contemporary herd average for the animal being evaluated. Although actual deviations could be used for expressing EBV, percentage deviations would be more useful for comparative purposes. This is due to the normal fluctuations from season to season and from year to year in herd average sow productivity levels.

In part A of equation [1], n is the number of records by the sow; k is the average number of records in the contemporary herd averages; h^2 is the estimated heritability of the sow

productivity index; s is the estimated average phenotypic correlation among contemporary herd records; and t is the estimated repeatability or average correlation among separate records of the sow. Recommended values for use in the equation are .20 for h^2, .30 for s, and .25 for t. The equation can then be expressed as follows:

$$\text{EBV (Sow)} = \frac{.2nk}{.7+.25k+.45nk} \overline{(\text{Sow} - \text{Herd average})}. \qquad [2]$$

In computing part B, we recommend that the contemporary herd average include contemporary records for all sows with which the particular sow is being compared, along with the record of the sow in question. For example, contemporary records for all sows of the same breed or strain would be used in computing the appropriate herd average with which each included record for the sow is compared.

Guidelines for Sows

(1) Specify contemporary herd average groups.

(2) Adjust all gilt litter indexes to a mature equivalent (M.E.) basis by multiplying the actual index by 1.15, an increase of 15 percent. This is a conservative adjustment based on the study by Lush and Molln (1942). Records for second and later farrowings would be used without further adjustment by the M.E. factor. All records would then be considered as being M.E.

(3) Compute contemporary herd average with M.E. records.

(4) Compute actual deviation of M.E. herd average from the sow's M.E. record.

(5) Convert actual deviation to percentage deviation.

(6) Compute the average of the sow's separate percentage deviations.

(7) Compute the sow's EBV with equation [2].

Examples of Computing Sow's EBV

Sow 1. Record 1, M.E. index = 76; M.E. herd average = 65; k = 15.

Actual deviation = 76-65 = +11.

Percentage deviation = $+11/65$ = +16.92%. n = 1.

$$\text{EBV (Sow 1)} = \frac{.2(1)(15)}{.7+.25(15)+.45(1)(15)} (+16.92\%) = .268(+16.92\%)$$

$$= +4.53\%.$$

Sow 2. Record 1, M.E. index = 46; M.E. herd average = 60; k = 12.

Actual deviation = 46-60 = -14.

Percentage deviation = $-14/60$ = -23.33%.

Record 2, M.E. index = 45; M.E. herd average = 55; k = 16.

Actual deviation = 45-55 = -10.

Percentage deviation = $-10/55$ = -18.18%.

Average percentage deviation = $1/2$ (-23.33-18.18) = -20.76%.

Average k = $1/2$ (12+16) = 14; n = 2.

$$\text{EBV (Sow 2)} = \frac{.2(2)(14)}{.7+.25(14)+.45(2)(14)} (-20.76\%) = .333(-20.76\%)$$

$$= -6.91\%.$$

Each sow's EBV would be updated as she completed an additional farrowing record in the herd.

Computing the Boar's EBV

The following equation is recommended:

$$\text{EBV (Boar)} = \underbrace{\frac{2\,N\,k\,h^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)}}_{A} \times \underbrace{(\text{Daughters} - \text{Herd averages})}_{B}. \qquad [3]$$

Part A is the regression factor used to derive an estimate of the sire's EBV from the average of his daughters' productivity indexes, each expressed as a percentage deviation from her contemporary herd average (part B), as described for the sow. In part A, N is the number of daughters included in the proof; k is the average number of sows included in the daughters' contemporary herd averages; h^2 and s are the same as described for sows; and e is the estimated environmental correlation among the tested daughters in the proof.

The following values are recommended for use in the equation: h^2 = .20, s = .30, and e = .05. Equation [3] can then be expressed as follows:

$$\text{EBV (Boar)} = \frac{.4Nk}{2.8+2.2k+.6Nk} \overline{\text{(Daughters - Herd averages)}}. \quad [4]$$

It should be noted that in equations [3] and [4] the daughters of the boar are assumed to be a mixture of half and full sibs. (See appendix for further explanation.)

Guidelines for Boars

(1) Compute the lifetime average percentage deviation of M.E. productivity indexes for each daughter of the boar being evaluated, as described under Guidelines for Sows in the previous section.

(2) Compute the average number of records (k) in the contemporary herd averages for each daughter.

(3) Compute the average of lifetime percentage deviations and average k among all daughters of the boar included in the proof.

(4) Compute the EBV for the boar with equation [4].

Examples of Computing Boar's EBV

Boar 1.
Daughter 1. Record 1, M.E. index = 57; M.E. herd average = 60; k = 20.

Actual deviation = 57-60 = -3.0; percentage deviation = $^{-3}/_{60}$ = -5.00%.

Record 2, M.E. index = 55; M.E. herd average = 50; k = 16.

Actual deviation = 55-50 = +5.0; percentage deviation = $^{+5}/_{50}$ = +10.00%.

Average percentage deviation for daughter 1 =
$\frac{1}{2}(-5.00+10.00) = +2.50\%$.

Average k for daughter 1 = $\frac{1}{2}(20+16) = 18$.

Daughter 2. Record 1, M.E. index = 46; M.E. herd average = 50;
k = 16.

Actual deviation = 46-50 = -4; percentage
deviation = $^{-4}/_{50}$ = -8.00%.

Record 2, M.E. index = 45; M.E. herd average = 55;
k = 20.

Actual deviation = 45-55 = -10; percentage
deviation = $^{-10}/_{55}$ = -18.18%.

Average percentage deviation for daughter 2 =
$\frac{1}{2}(-8.00-18.18) = -13.09\%$.

Average k for daughter 2 = $\frac{1}{2}(16+20) = 18$.

Daughter 3. Record 1, M.E. index = 50; M.E. herd average = 55;
k = 20.

Actual deviation = 50-55 = -5.0; percentage
deviation = $^{-5}/_{55}$ = -9.09%.

Daughter 4. Record 1, M.E. index = 51; M.E. herd average = 55;
k = 20.

Actual deviation = 51-55 = -4.0; percentage
deviation = $-^{4}/_{55}$ = -7.27%.

Daughter 5. Record 1, M.E. index = 40; M.E. herd average = 55;
k = 20.

Actual deviation = 40-55 = -15; percentage
deviation = $-^{15}/_{55}$ = -27.27%.

Daughter 6. Record 1, M.E. index = 65; M.E. herd average = 55;
k = 20.

Actual deviation = 65-55 = +10; percentage
deviation = $+^{10}/_{55}$ = +18.18%.

Average percentage for 6 daughters
= $\frac{1}{6}(+2.50-13.09-9.09-7.27-27.27+18.18)$
= $\frac{1}{6}(-36.04)$ = -6.01%.

Average k for 6 daughters = $\frac{1}{6}(18+18+20+20+20+20)$ = 19.33; N = 6.

$$\text{EBV (Boar 1)} = \frac{.4(6)(19.33)}{2.8+2.2(19.33)+.6(6)(19.33)}(-6.01\%)$$

$$= .404(-6.01\%) = -2.43\%.$$

Boar 2.

Daughter 1. Record 1, M.E. index = 60; M.E. herd average = 50; k = 12.

Actual deviation = 60-50 = +10; percentage deviation = $^{+10}/_{50}$ = +20.00%.

Daughter 2. Record 1, M.E. index = 55; M.E. herd average = 50; k = 12.

Actual deviation = 55-50 = +5.0; percentage deviation = $^{+5}/_{50}$ = +10.0%.

Daughter 3. Record 1, M.E. index = 65; M.E. herd average = 50; k = 12.

Actual deviation = 65-50 = +15; percentage deviation = $^{+15}/_{50}$ = +30.0%.

Daughter 4. Record 1, M.E. index = 50; M.E. herd average = 50; k = 12.

Actual deviation = 50-50 = 0; percentage deviation = 0%.

Average percentage deviation for 4 daughters = $\frac{1}{4}(+20+10+30+0)$ = +15.0%.

Average k for 4 daughters = 12; N = 4.

$$\text{EBV (Boar 2)} = \frac{.4(4)(12)}{2.8+2.2(12)+.6(4)(12)}(+15.0\%) = .331(+15.0\%)$$

$$= +4.96\%.$$

Boar 3. No proof yet available. Sire of Boar 3 = Boar 2; Dam = Sow 1.

Boar 4. No proof available; no proof available for Sire of Boar 4; Dam = Sow 2.

Computing EBV
for Young
Breeding Herd
Candidates

Sow and boar EBV's referred to here are those in the previous sections.

Candidate 1 (C1):   Sire = Boar 1; Dam = Sow 1.

$$EBV(C1) = \frac{1}{2}[EBV(Boar\ 1)+EBV(Sow\ 1)]$$

$$= \frac{1}{2}(-2.43+4.53) = +1.05\%.$$

C2:   Sire = Boar 2; Dam = Sow 2.

$$EBV(C2) = \frac{1}{2}[EBV(Boar\ 2)+EBV(Sow\ 2)]$$

$$= \frac{1}{2}(+4.96-6.91) = -.98\%.$$

C3:   Sire = Boar 3 (no proof); Dam = Sow 2.

Boar 3 has Boar 2 as his Sire and Sow 1 as his Dam.

$$EBV(Boar\ 3) = \frac{1}{2}[EBV(Boar\ 2)+EBV(Sow\ 1)]$$

$$= \frac{1}{2}(+4.96+4.53) = +4.74\%.$$

$$EBV(C3) = \frac{1}{2}[EBV(Boar\ 3)+EBV(Sow\ 2)]$$

$$= \frac{1}{2}(+4.74-6.91) = -1.08\%.$$

C4:   Sire = Boar 4 (no proof); Dam = Sow 1.

Boar 4's Sire also has no proof; Boar 4's Dam = Sow 2.

$$EBV(C4) = \frac{1}{2}[\frac{1}{2}EBV(Sow\ 2)+EBV(Sow\ 1)]$$

$$= \frac{1}{2}[\frac{1}{2}(-6.91)+4.53] = +.54\%.$$

Applying the
Procedures

The procedures recommended here are designed primarily for within-herd selection purposes and therefore are applicable mainly in stabilized breeding situations. These include systems of traditional purebred breeding, developing specialized sire and dam breeds or strains, breeding within a strain formed by crossing two or more breeds, and rotational cross breeding. In these systems, young breeding herd candidates would probably also be tested for such performance traits as rate of gain, feed conversion, and backfat thickness. Each candidate's EBV for sow productivity would be considered, along with its own performance record, in determining an overall index combining the separate traits. The comparative emphasis to put on the separate traits in the combined index would depend on the particular usage or function for which the

breed, strain, or cross was being developed. Guidelines for such a combined selection index are beyond the scope of this publication.

It is also important to note that comparisons of animals between herds, even on the basis of EBV, should only be done with extreme care because of possibly significant differences in management, facilities, or genetic merit.

Use of Computers
With the increasing use of computers on the farm, many producers will be able to develop their own computer programs to evaluate the animals in their breeding herds along the lines proposed here. In addition, commercial and public extension facilities probably will become available or expanded so as to provide the services needed to evaluate animals in subscriber herds along the lines proposed here.

Further Research Needs
It should be emphasized that the proposed procedures are neither exact nor ideal. As a result, large standard errors are probably associated with each EBV. Further research is needed to obtain more reliable estimates of the basic parameters used in the various equations and to increase the computational capabilities to derive those estimates.

However, in the meantime, it should be recognized that the recommended procedures represent substantial improvement in the evaluation of genetic merit for sow productivity in young breeding herd candidates--both boars and gilts. Major improvements from past practices are the inclusion of information from the sire's side of the pedigree and consideration of nongenetic effects in the basic equations. Thus, though all the theoretical assumptions have not been strictly adhered to, the consequences are not considered to be serious enough to prevent applying the proposed guidelines for their intended usage.

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APPENDIX

The following derivations of equations involving EBV are based on traditional animal breeding theory and on publications by Wright (1934) and Touchberry (1961).

Sow EBV

Figure 1 is the pertinent path diagram for use in deriving the expected correlation (R) of the true breeding value of a sow with its estimated breeding value (EBV) based on its own productivity records. (See fig. 1 for description of various letters used here.)

$$R_{G_{\text{Sow}}} (\overline{S-HA}) = n\ h\ o\ p.$$

$$o = \frac{\sigma_S}{\sigma_{(S-HA)}}; \quad p = \sqrt{\frac{1}{n[1+(n-1)r_{(S-HA)_i\ (S-HA)_j}]}}.$$

(n is the number of records by the sow; σ is a symbol for standard deviation, the square root of variance; r is a general symbol for correlation; $\sqrt{}$ is a symbol for square root.)
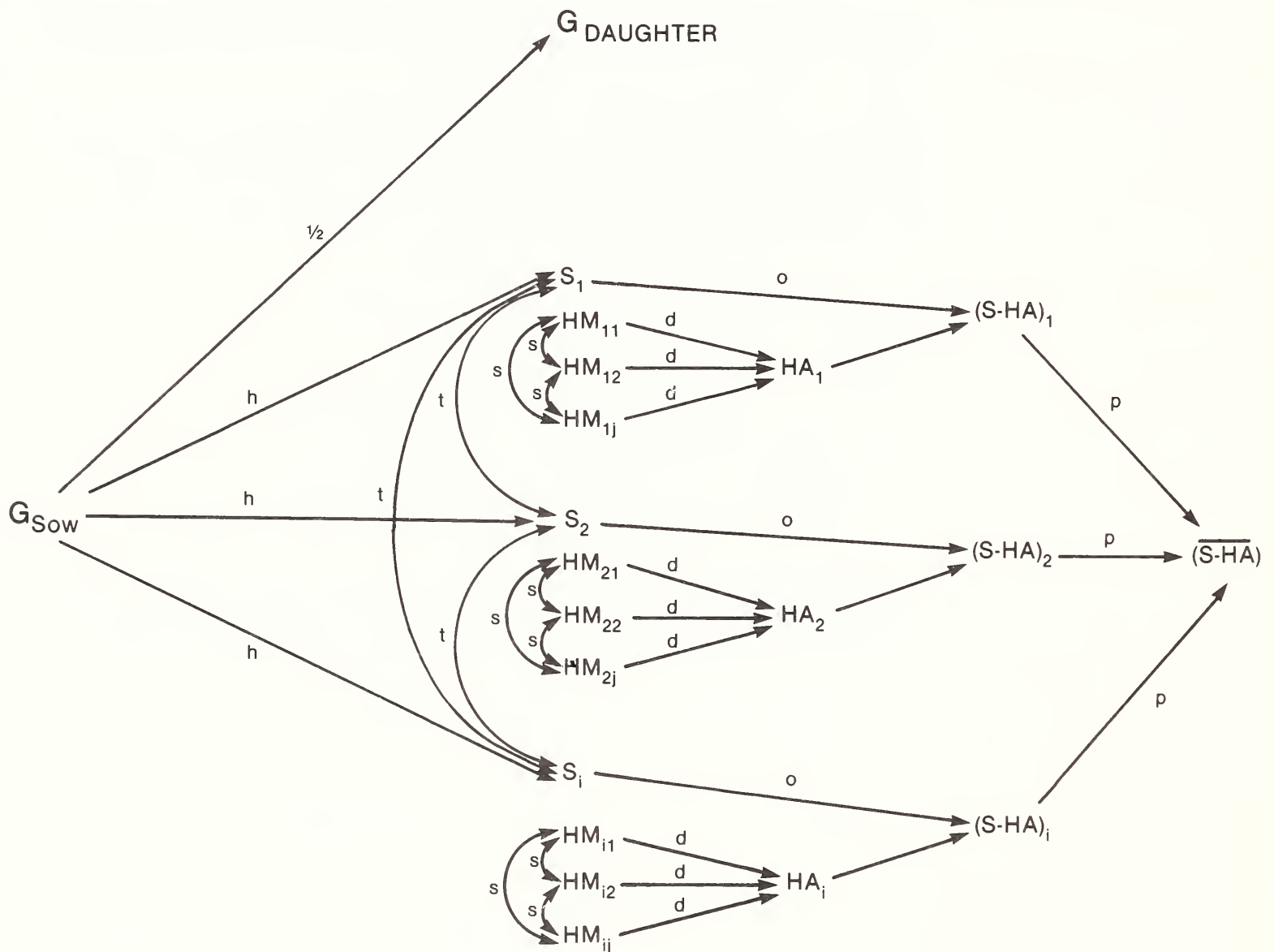
To evaluate o:

$$\sigma^2_{(S-HA)} = \sigma^2_S + \sigma^2_{HA} - 2\sigma_S\ \sigma_{HA}r_{S,HA};$$

$$\sigma^2_{HA} = \sigma^2_S \left[\frac{1+(k-1)s}{k}\right]; \quad \text{assume } \sigma^2_S = \text{variance among herdmates;}$$

$$\therefore \sigma^2_{(S-HA)} = \sigma^2_S + \sigma^2_S \left[\frac{1+(k-1)s}{k}\right]$$

$$-2\sigma_S \left[\sigma_S \sqrt{\frac{1+(k-1)s}{k}}\right] r_{S,HA}.$$

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Figure 1

Path Diagram Showing Relationship Between G_{Sow} and $(\overline{S\text{-}HA})$
(Modified From Touchberry, 1961)

$G_{DAUGHTER}$

G_{Sow}

½

h

h

h

t

t

t

S_1 o $(S\text{-}HA)_1$

HM_{11} d

s

HM_{12} d HA_1

s

HM_{1j} d

p

S_2 o $(S\text{-}HA)_2$ p

HM_{21} d

s

HM_{22} d HA_2

s

HM_{2j} d

$(\overline{S\text{-}HA})$

S_i o

HM_{i1} d

s

HM_{i2} d HA_i

s

HM_{ij} d

$(S\text{-}HA)_i$

p

G = genetic merit or true breeding value of an animal.

S_i = sow's i^{th} record or phenotype.

HM_{ij} = j^{th} herdmate of sow's i^{th} record.

HA_i = herdmate average for sow's i^{th} record.

$(S\text{-}HA)_i$ = deviation of herdmate average from sow's i^{th} record.

$(\overline{S\text{-}HA})$ = average of (S-HA) for all sow's records.

h = square root of heritability.

o = path coefficient from S_i to $(S\text{-}HA)_i$.

p = path coefficient from (S-HA) to $(\overline{S\text{-}HA})$.

d = path coefficient from HM_{ij} to HA_i.

s = phenotypic correlation among contemporary herdmates.

t = phenotypic correlation among different records for sow.

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($\dot{\sigma}^2$ is a symbol for variance; k is the number of herdmates; $\therefore$ is a symbol for "therefore.")

$$r_{S,HA} = ksd; \quad d = \frac{\sigma_{HM}}{\sigma_{HA}} = \sqrt{\frac{1}{k[1+(k-1)s]}} \cdot$$

$$r_{S,HA} = ks\sqrt{\frac{1}{k[1+(k-1)s]}} = s\sqrt{\frac{k}{1+(k-1)s}}$$

$$\text{and} \quad \sigma^2(S-HA) = \sigma^2 S + \sigma^2 S\left[\frac{1+(k-1)s}{k}\right]$$

$$-2\sigma_S\left[\sigma_S\sqrt{\frac{1+(k-1)s}{k}}\right]\left[s\sqrt{\frac{k}{1+(k-1)s}}\right]$$

$$= \sigma^2 S\left\{1+\left[\frac{1+(k-1)s}{k}\right] - 2s\right\} \cdot$$

$$\text{So,} \quad \sigma(S-HA) = \sigma_S\sqrt{1+\frac{1+(k-1)s}{k}-2s} = \sigma_S\sqrt{\frac{(1-s)(k+1)}{k}} \cdot [5]$$

$$o = \frac{\sigma_S}{\sigma(S-HA)} = \frac{\sigma_S}{\sigma_S\sqrt{\frac{(1-s)(k+1)}{k}}} = \sqrt{\frac{k}{(1-s)(k+1)}} \cdot$$

$$r_{(S-HA)_i (S-HA)_j} = h^2o^2+o^2t = o^2(h^2+t).$$

$$\therefore r_{(S-HA)_i (S-HA)_j} = \left[\frac{k}{(1-s)(k+1)}\right](h^2+t) \qquad [6]$$

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$$\text{and } p = \sqrt{\dfrac{1}{n\left\{1+(n-1)\left[\dfrac{k(h^2+t)}{(1-s)(k+1)}\right]\right\}}}$$

$$= \sqrt{\dfrac{(1-s)(k+1)}{n[(1-s)(k+1)+(n-1)k(h^2+t)]}} \;.$$

Thus, $^R G_{Sow}\;\overline{(S-HA)} = nh\sqrt{\dfrac{k}{(1-s)(k+1)}}\quad \text{X}$

$$\sqrt{\dfrac{(1-s)(k+1)}{n[(1-s)(k+1)+(n-1)k(h^2+t)]}}$$

$$= \sqrt{\dfrac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}}\;.$$

Next, the regression (b) of the sow's true breeding value on her own productivity records is derived as follows:

$$^b G_{Sow}\;\overline{(S-HA)} = {}^R G_{Sow}\;\overline{(S-HA)}\;\dfrac{\sigma\,G_{Sow}}{\sigma\,\overline{(S-HA)}}\;.$$

$$\sigma\,\overline{(S-HA)} = \sigma\,(S-HA)\sqrt{\dfrac{1+(n-1)r_{(S-HA)_i(S-HA)_j}}{n}}\;.$$

From equation [5], $\sigma\,(S-HA) = \sigma\,S\sqrt{\dfrac{(1-s)(k+1)}{k}}$

and from equation [6], $r_{(S-HA)_i (S-HA)_j} = \left[\dfrac{k}{(1-s)(k+1)} \right] (h^2+t)$.

$$\therefore \sigma_{(\overline{S-HA})} = \sigma_S \sqrt{\dfrac{(1-s)(k+1)}{k}} \sqrt{\dfrac{1+(n-1)\left[\dfrac{k(h^2+t)}{(1-s)(k+1)}\right]}{n}}$$

$$= \sigma_S \sqrt{\dfrac{(1-s)(k+1)+(n-1)k(h^2+t)}{nk}} \ .$$

$$\dfrac{\sigma_{G_{Sow}}}{\sigma_S} = h; \qquad \sigma_{G_{Sow}} = h \ \sigma_S \ .$$

$$\therefore \dfrac{\sigma_{G_{Sow}}}{\sigma_{(\overline{S-HA})}} = \dfrac{h \ \sigma_S}{\sigma_S \sqrt{\dfrac{(1-s)(k+1)+(n-1)k(h^2+t)}{nk}}}$$

$$= \sqrt{\dfrac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}} \ .$$

$$\therefore \ ^b G_{Sow}(\overline{S-HA}) = \sqrt{\dfrac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}} \ \ X$$

$$\sqrt{\dfrac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}}$$

$$\text{and } \ ^b G_{Sow}(\overline{S-HA}) = \dfrac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} \ .$$

$$\text{EBV(Sow)} = {}^{b}G_{\text{Sow}} \; \overline{(\text{S--HA})} \; \overline{(\text{Sow} - \text{Herd average})}$$

$$= \frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} \; \overline{(\text{Sow} - \text{Herd average})}.$$

From figure 1,

$${}^{R}G_{\text{Progeny}} \; \overline{(\text{Dam--HA})} = \frac{1}{2} \; {}^{R}G_{\text{Sow}} \; \overline{(\text{S--HA})}$$

$$= \frac{1}{2} \sqrt{\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}}. \qquad [7]$$

It can also be shown that

$${}^{b}G_{\text{Progeny}} \; \overline{(\text{Dam--HA})} = \frac{1}{2} \; {}^{b}G_{\text{Sow}} \; \overline{(\text{S--HA})}$$

$$= \frac{1}{2} \; \frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}. \qquad [8]$$

Also, where PGD = paternal granddam,

$${}^{R}G_{\text{Progeny}} \; \overline{(\text{PGD--HA})} = \frac{1}{4} \; {}^{R}G_{\text{Sow}} \; \overline{(\text{S--HA})}$$
.

$$= \frac{1}{4} \sqrt{\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}} .$$

Furthermore, it can be shown that

$$^{b}G_{Progeny} \, \overline{(PGD-HA)} = \frac{1}{4} \, ^{b}G_{Sow} \, \overline{(S-HA)}$$

$$= \frac{1}{4} \frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} .$$

Boar EBV

Figure 2 is the pertinent path diagram for use in deriving the expected correlation (R) of the true breeding value of a boar with his estimated breeding value (EBV) based on the productivity records of his tested daughters (D) in the herd. See figure 2 for description of letters used here.

The equations for $^{R}G_{Boar} \, (\overline{D-HA})$ and $^{b}G_{Boar} \, (\overline{D-HA})$ are derived similarly to those for $^{R}G_{Sow} \, (\overline{S-HA})$ and $^{b}G_{Sow} \, (\overline{S-HA})$ in the previous section. One change involves $^{r}(D-HA)_i(D-HA)_j$ in comparison with $^{r}(S-HA)_i(S-HA)_j$.
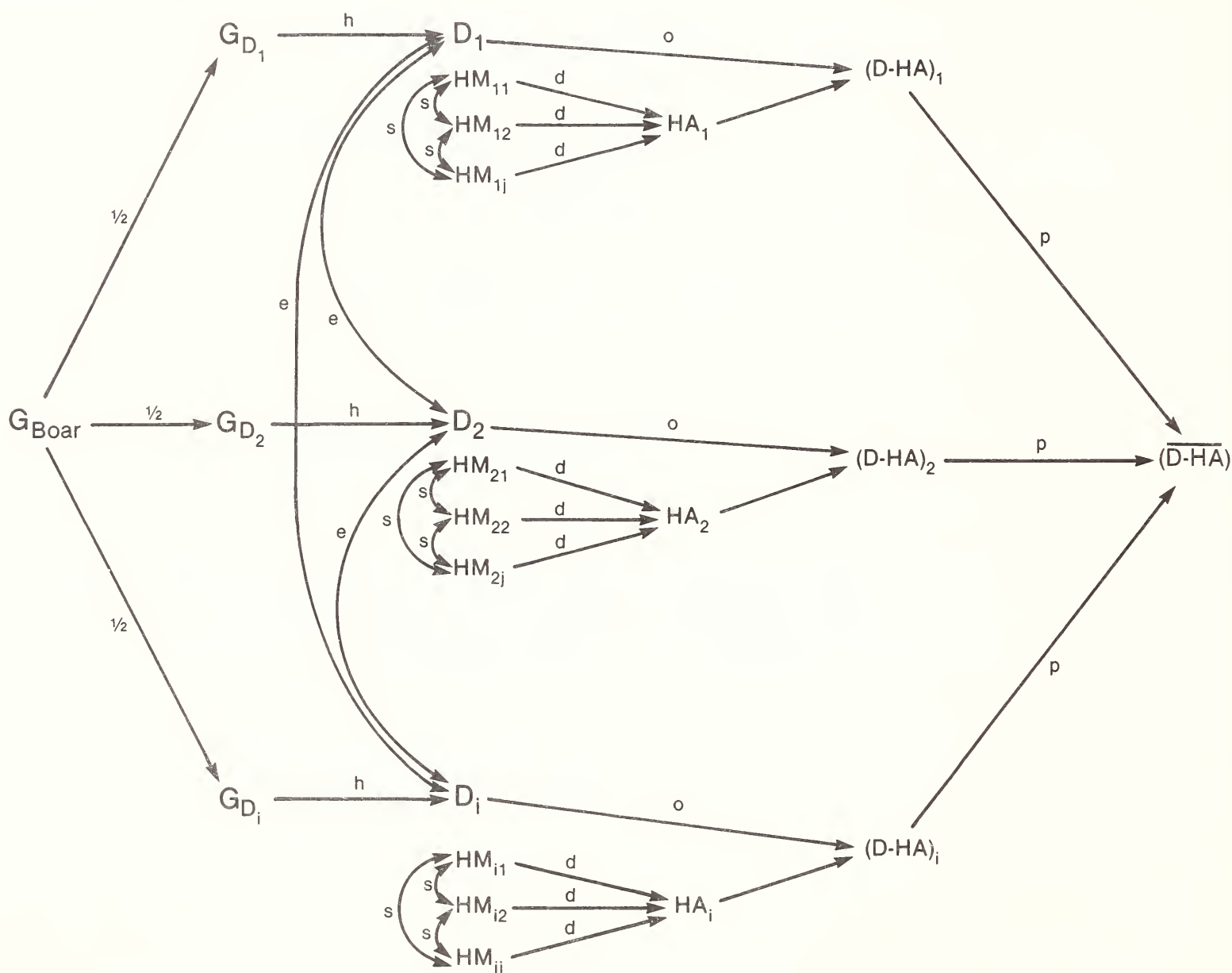
$$^{r}(D-HA)_i(D-HA)_j = \frac{h^2}{4} o^2 + o^2 e = o^2 \frac{(h^2+4e)}{4}$$

$$= \frac{k}{(1-s)(k+1)} \frac{h^2+4e}{4} ,$$

where o was derived in the previous section for Sow EBV.

Another change is that N is the number of tested daughters of the boar, whereas n was the number of records by the sow.

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Figure 2

Path Diagram Showing Relationship Between G_{Boar} and $(\overline{D\text{-}HA})$
(Modified From Touchberry, 1961)

G = genetic merit or true breeding value of an animal.

D_i = i^{th} daughter's record or phenotype.

HM_{ij} = j^{th} herdmate of ith daughter.

HA_i = herdmate average for i^{th} daughter.

$(D\text{-}HA)_i$ = deviation of herdmate average from record for i^{th} daughter.

$(\overline{D\text{-}HA})$ = average of (D-HA) for all daughters of boar.

h = square root of heritability.

o = path coefficient from D_i to $(D\text{-}HA)_i$.

p = path coefficient from (D-HA) to $(\overline{D\text{-}HA})$.

d = path coefficient from HM_{ij} to HA_i.

s = phenotypic correlation among contemporary herdmates.

e = nongenetic correlation among daughters of a boar.

As a result, $^{R}G_{Boar}$ $(\overline{D-HA})$ = $\sqrt{\dfrac{Nkh^2}{4(1-s)(k+1)+k(N-1)(h^2+4e)}}$

and $^{b}G_{Boar}$ $(\overline{D-HA})$ = $\dfrac{2Nkh^2}{4(1-s)(k+1)+k(N-1)(h^2+4e)}$.

These two equations assume that all daughters are half sibs.
For the situation where all daughters are full sibs,

$$r(D-HA)_i(D-HA)_j = \underbrace{\dfrac{h^2}{4}o^2 + o^2e}_{\substack{\text{through} \\ \text{the sire}}} + \underbrace{\dfrac{h^2}{4}o^2 + o^2e}_{\substack{\text{through} \\ \text{the dam}}}$$

$$= \dfrac{2o^2(h^2+4e)}{4} = \dfrac{k(h^2+4e)}{2(1-s)(k+1)} .$$

∴ With full-sib daughters,

$^{R}G_{Boar}(\overline{D-HA})$ = $\sqrt{\dfrac{Nkh^2}{4(1-s)(k+1)+2k(N-1)(h^2+4e)}}$

and $^{b}G_{Boar}$ $(\overline{D-HA})$ = $\dfrac{2Nkh^2}{4(1-s)(k+1)+2k(N-1)(h^2+4e)}$.

Similarly, when the daughters are an equal mixture of half and full sibs, it can be shown that

$$R_{G_{Boar}} (\overline{D-HA}) = \sqrt{\frac{Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)}} \qquad [9]$$

$$\text{and } {}^b G_{Boar} (\overline{D-HA}) = \frac{2Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)} \cdot \qquad [10]$$

Since in most practical situations, it is likely that the tested daughters of the boar will be a mixture of half and full sibs, equation [9] would be the most appropriate one to use in computing the boar's EBV. Therefore,

$$R_{G_{Progeny}} \text{ (sire proof)} = \frac{1}{2} R_{G_{Boar}} (\overline{D-HA})$$

$$= \frac{1}{2} \sqrt{\frac{Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)}}$$

and

$$^b G_{Progeny} \text{ (sire proof)} = \frac{1}{2} {}^b G_{Boar} (\overline{D-HA})$$

$$= \frac{1}{2} \frac{2Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)} \cdot$$

Also,

$$R_{G_{Progeny}} \text{ (PGS proof)} = \frac{1}{4} R_{G_{Boar}} (\overline{D-HA})$$

$$= \frac{1}{4} \sqrt{\frac{Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)}}$$

and

$$^{b}G_{Progeny} \text{ (PGS proof)} = \frac{1}{4} \; ^{b}G_{Boar} \; \overline{(D-HA)}$$

$$= \frac{1}{4} \; \frac{2Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)} \; .$$

Computing R-Values for Tables 1 and 2

The following equations were used, based on Henderson (1963):

For table 1, part I, equation [7] for $^{R}G_{Progeny} \overline{\text{(Dam-HA)}}$ was used.

For table 1, part II, the following equation was used:

$$^{R}G_{Progeny} \text{ (Dam + Sire)} = \frac{1}{2} \sqrt{^{b}G_{Progeny} \overline{\text{(Dam-HA)}} + \frac{1}{2} \; ^{b}G_{Progeny} \text{ (sire proof)}}$$

$$= \frac{1}{2} \sqrt{\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} + \frac{2Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)}} \; . \quad [11]$$

For table 1, part III, the following equation was used:

$$R_{G_{Progeny} (Dam+PGD+PGS)} = \sqrt{\frac{1}{2}\, {}^{b}G_{Progeny}\,\overline{(Dam-HA)} + \frac{1}{4}\, {}^{b}G_{Progeny}\overline{(PGD-HA)} + \frac{1}{4}\, {}^{b}G_{Progeny}(PGS\ proof)}$$

$$= \sqrt{\frac{1}{2}\,\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} + \frac{1}{4}\,\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} + \frac{1}{4}\,\frac{2Nkh^2}{4(1-s)(k+1)+1.5k(N-1)(h^2+4e)}}\ .[12]$$

For table 2, equation [9] for $R_{G_{Boar}}\overline{(D-HA)}$ was used.

$$R_{G_{Progeny} (Dam + PGD)} = \frac{1}{2}\sqrt{\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)} + \frac{1}{4}\,\frac{nkh^2}{(1-s)(k+1)+k(n-1)(h^2+t)}}\ . \qquad [13]$$

Basic
Assumptions

In deriving the expected correlation of the true breeding value of dairy bulls with their EBV's based on proofs of their daughter-herdmate comparisons, Touchberry (1961) listed several assumptions for his biometrical model. Key among these were the following:

(1) Bulls were mated to a random group of cows in the herd.

(2) Tested daughters included in the proof were not selected.

(3) No bull included as sire of a group of daughters was also a sire of a herdmate.

These same basic assumptions would also apply to the comparable correlations and regressions presented here for evaluating sows and boars. However, assumption (3) was relaxed here mainly for practical reasons to facilitate computations on the farm. Thus, the sow's record was included in her contemporary herd average. Also, records of the boar's daughters were included in their contemporary herd averages.

Although such inclusions might tend to bias the resultant EBV, any such bias might be counterbalanced by the added information included in the herd averages. The net result would be more precise estimates of herd environmental effects that are used in the deviations to obtain more accurate estimates of breeding value.

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